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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Sunil Kumar VERMA, et al

Serial No.: 09/821,782 Group No.:

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For: UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

Attorney Docket No.: U 013365-9

Assistant Commissioner for Patents
Washington, DC 20231

PRELIMINARY AMENDMENT

IN THE SPECIFICATION:

Please replace the paragraph beginning at page 5, line 28, with:

Figures 1A-1D illustrate the step-wise procedure involved in analyses. The unknown biological material i.e. 'Adil.flesh' refers to the confiscated skin mentioned in 'Example 6'. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin `adil.flesh' was subjected to DNA isolation using the standard procedures[74]. The DNA obtained was amplified using the primers `mcb398' and `mcb869' in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA).

CERTIFICATE OF MAILING (37 CFR 1.8a)

I hereby certify that this paper (along with any paper referred to as being attached or enclosed) is being deposited with the United States Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed to the: Commissioner of Patents and Trademarks, Washington, DC 20231

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The lane `M' shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from `adil.flesh' using primers `mcb398' and `mcb869'. The PCR amplicon obtained were sequenced at both the strand using "ABI Prism 3700 DNA Analyzes, PE-Applied Biosystems). The chromatogram shows the sequences (about 80 by long, i.e. between 150-230 by of sequence (328 bp), revealed from the PCR product of 472 by length) obtained from `adil.flesh'.

Figures 1E-1H illustrate the further steps involved in *analyses*. The sequence (328 bp) revealed from `adil.flesh' was subjected to homology search in *nr* (i.e. non-redundant) database of Netional Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 by sequence from adil.flesh) and the sequences registered in *nr* database of NCBI. BLAST analysis revealed the highest homology of the sequence revealed from `adil.flesh' with the sequence of *Panthera pardus* (gene bank registration number `AY005809'), indicating the identity of adil.flesh as that of a leopard (*Panthera pardus*) origin. Figure lb further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from 'adil.flesh'. The sequences of `adil.flesh' is similar to the sequences of `gz1L' further confirming the identity of the source of confiscated remain `adil.flesh' as that of a *Panthera pardus* origin.

Figure l I illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from `adil.flesh' and reference animals listed in Table 5. The animals belonging to similar species cluster together; however, the animals of different species group in different clusters.

The confiscated material under investigation (i.e. `adil.flesh') clusters with `gz1L' (i.e. the known normal leopard '*Panthera pardus*') indicating the identity of the species of `adil.flesh' as that of a *Panthera pardus* source.

Page 326, after last line of Table 12 insert the following Sequence Listing: